

Fri Dec 3 11:48:18 2004

10024369-3_1018-1037sl.rnpb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:43:49 ; Search time 0.001 Seconds
(without alignments)
21.120 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20
Sequence: 1 cttctgcccaagaagtcg99 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 50 segs, 528 residues

Total number of hits satisfying chosen parameters: 100

Minimum DB seg length: 8
Maximum DB seg length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 50 summaries

Database : rnpbdb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	1	US-10-024-369-47
2	12.8	64.0	17	1	Sequence 47, Appl
3	12.8	64.0	17	1	Sequence 674, App
4	12	60.0	15	1	Sequence 674, App
5	12	60.0	15	1	Sequence 2, Appli
6	9.4	47.0	12	1	Sequence 445, App
7	9	45.0	10	1	Sequence 410, App
8	9	45.0	10	1	Sequence 930, App
9	9	45.0	10	1	Sequence 1231, Ap
10	9	45.0	10	1	Sequence 15, Appl
11	8.4	42.0	10	1	Sequence 262, App
12	8.4	42.0	10	1	Sequence 437, App
13	8.4	42.0	10	1	Sequence 2081, Ap
14	8.4	42.0	10	1	Sequence 3, Appli
15	8.4	42.0	10	1	Sequence 713, App
16	8.4	42.0	10	1	Sequence 330, App
17	8.4	42.0	10	1	Sequence 84, Appl
18	8.4	42.0	10	1	Sequence 398, App
19	8.4	42.0	11	1	Sequence 73, Appl
20	8.4	42.0	11	1	Sequence 170, App
21	8.4	42.0	11	1	Sequence 1253, Ap
22	8.4	42.0	11	1	Sequence 1259, Ap
23	8.4	42.0	11	1	Sequence 2078, Ap
24	8.4	42.0	9	1	Sequence 2079, Ap
25	8.4	42.0	9	1	Sequence 2262, Ap
26	8.4	42.0	9	1	Sequence 2263, Ap
27	8.4	42.0	9	1	Sequence 2078, Ap
28	8.4	42.0	9	1	Sequence 2079, Ap
29	8.4	42.0	9	1	Sequence 2262, Ap
30	8.4	42.0	9	1	Sequence 2263, Ap
31	8.4	42.0	9	1	Sequence 2078, Ap
32	8.4	42.0	9	1	Sequence 2079, Ap
33	8.4	42.0	9	1	Sequence 2262, Ap

34	8	40.0	9	1	US-09-989-994-2079	Sequence 2079, Ap
35	8	40.0	9	1	US-09-989-994-2262	Sequence 2262, Ap
36	8	40.0	9	1	US-09-989-994-2263	Sequence 2263, Ap
37	8	40.0	9	1	US-10-006-069A-7	Sequence 7, Appli
38	8	40.0	10	1	US-10-033-145-198	Sequence 198, App
39	8	40.0	10	1	US-10-033-145-199	Sequence 298, App
40	8	40.0	10	1	US-10-033-145-298	Sequence 298, App
41	8	40.0	10	1	US-10-033-145-701	Sequence 701, App
42	8	40.0	10	1	US-10-033-145-1370	Sequence 1370, Ap
43	8	40.0	10	1	US-10-033-145-1792	Sequence 1792, Ap
44	8	40.0	10	1	US-10-033-145-1806	Sequence 1806, Ap
45	8	40.0	10	1	US-10-033-145-1979	Sequence 1979, Ap
46	8	40.0	10	1	US-10-010-802-281	Sequence 281, App
47	8	40.0	10	1	US-10-330-627-132	Sequence 132, App
48	8	40.0	10	1	US-10-330-627-1157	Sequence 1157, Ap
49	8	40.0	10	1	US-10-293-222-324	Sequence 324, App
50	8	40.0	10	1	US-10-215-982-360	Sequence 360, App

ALIGNMENTS

RESULT 1
US-10-024-369-47/c
Publication No. US20030134809A1
GENERAL INFORMATION:
APPLICANT: Alexander H. Borchers
APPLICANT: Donna T. Ward
TITLE OF INVENTION: ANTISENSE MODULATION OF ABC TRANSPORTER MHC 1 EXPRESSION
FILE REFERENCE: RTS-0353
CURRENT APPLICATION NUMBER: US/10/024,369
CURRENT FILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 91
SEQ ID NO 47
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-10-024-369-47

Query Match 100.0%; Score 20; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.097;
Matches 20; Conservativity 0; Mismatches 0; Indels 0; Gaps 0;
QY 1018 CTTCTGCCCAAGAAGTGGG 1037
DB 20 CTTCTGCCCAAGAAGTGGG 1

RESULT 2
US-09-930-423-674
Sequence 674, Application US/09930423
Publication No. US20030092003A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blact, Larry
TITLE OF INVENTION: Method and Reagent for the Treatment of Alzheimer's Disease
FILE REFERENCE: MEMB00_918-A_400/027
CURRENT APPLICATION NUMBER: US/09/930,423
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 4553
SOFTWARE: PatentIn version 3.0
SEQ ID NO 674
LENGTH: 17
TYPE: RNA
ORGANISM: Homo Sapiens
US-09-930-423-674
Query Match 64.0%; Score 12.8; DB 1; Length 17;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:41:56 ; Search time 0.001 Seconds
(without alignments)

14.120 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20

Sequence: 1 cttctgcccagaagatg99 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 36 segs, 353 residues

Total number of hits satisfying chosen parameters: 72

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Database : rn1db:*
Listing first 36 summaries

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	45.0	11	US-09-862-847-15	Sequence 15, Appl
2	45.0	12	US-09-862-844-6	Sequence 6, Appl
3	45.0	12	US-09-862-844-8	Sequence 8, Appl
4	42.0	10	US-08-410-7798-47	Sequence 47, Appl
5	42.0	10	US-09-508-7538-225	Sequence 225, App
6	42.0	10	PCT-US95-04477-47	Sequence 47, Appl
7	42.0	11	US-08-401-512-15	Sequence 15, Appl
8	42.0	11	US-08-481-6588-73	Sequence 73, Appl
9	42.0	11	US-08-477-504A-73	Sequence 73, Appl
10	42.0	11	US-08-486-756A-73	Sequence 73, Appl
11	42.0	11	US-08-485-862B-73	Sequence 73, Appl
12	42.0	11	US-08-787-739-73	Sequence 73, Appl
13	42.0	11	US-08-487-077A-73	Sequence 73, Appl
14	42.0	11	US-08-485-863A-73	Sequence 73, Appl
15	42.0	11	US-08-485-049D-73	Sequence 73, Appl
16	42.0	11	US-09-178-115-73	Sequence 73, Appl
17	42.0	11	US-09-177-776-73	Sequence 73, Appl
18	42.0	11	US-09-772-719B-73	Sequence 73, Appl
19	40.0	10	US-08-049-283A-31	Sequence 31, Appl
20	40.0	10	US-08-049-283A-33	Sequence 33, Appl
21	40.0	10	US-09-508-753B-70	Sequence 70, Appl
22	37.0	9	US-08-437-013-6	Sequence 6, Appl
23	37.0	9	US-09-275-506A-6	Sequence 6, Appl
24	35.0	9	US-09-639-576-2	Sequence 2, Appl
25	35.0	8	US-08-593-345B-19	Sequence 19, Appl
26	35.0	8	US-08-859-954-55	Sequence 55, Appl
27	35.0	8	US-08-859-954-248	Sequence 248, App
28	35.0	8	US-08-859-954-249	Sequence 249, App
29	35.0	8	US-08-859-954-267	Sequence 267, App
30	35.0	8	US-08-859-954-406	Sequence 406, App
31	35.0	8	US-08-859-954-540	Sequence 540, App
32	35.0	8	US-08-855-372B-6	Sequence 6, Appl
33	35.0	8	US-09-498-851-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-862-847-15/c
Sequence 15, Application US/09862844
Patent No. 6593111
GENERAL INFORMATION:
APPLICANT: Baric, Ralph S.
APPLICANT: Boyd, Yount
TITLE OF INVENTION: DIRECTION ASSEMBLY OF LARGE VIRAL GENOMES AND CHROMOSOMES
FILE REFERENCE: 5470.270
CURRENT APPLICATION NUMBER: US/09/862,847
CURRENT FILING DATE: 2001-05-21
PRIOR APPLICATION NUMBER: US 60/206,537
PRIOR FILING DATE: 2000-05-21
PRIOR APPLICATION NUMBER: US 60/285,320
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 11
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide primer.
US-09-862-847-15

Query Match
Best Local Similarity 45.0%; Score 9; DB 1; Length 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1033 CCAGAGAG 1033
Db 10 CCAGAGAG 2
RESULT 2
US-09-862-844-6/c
Sequence 6, Application US/09862844
Patent No. 6583986
GENERAL INFORMATION:
APPLICANT: Cai, Hong
APPLICANT: Keller, Richard
APPLICANT: Werner, James
APPLICANT: Goodwin, Peter
TITLE OF INVENTION: RAPID HAPLOTYPE BY SINGLE MOLECULE DETECTION
FILE REFERENCE: S-94,652
CURRENT APPLICATION NUMBER: US/09/862,844
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 12
TYPE: DNA
ORGANISM: PNA probe MLGcysp
US-09-862-844-6

Query Match
Best Local Similarity 45.0%; Score 9; DB 1; Length 12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1033 GCCCAGAGA 1031
Db 10 GCCCAGAGA 2

RESULT 3

```

107 8.4 42.0 11 1 ABO66415 Human skin stress/
108 8.4 42.0 11 1 ABV6344 Human skin EST 413
109 8.4 42.0 11 1 ABV62764 Human skin EST 550
110 8.4 42.0 11 1 ABV70185 Human skin EST 797
111 8.4 42.0 11 1 ABV62651 Human skin EST 437
112 8.4 42.0 11 1 ABV67006 Human skin EST 479
113 8.4 42.0 11 1 ABV67047 Human skin EST 483
114 8.4 42.0 11 1 ABV64836 Human skin EST 262
115 8.4 42.0 11 1 ABV67092 Human skin EST 487
116 8.4 42.0 11 1 ABV67518 Human skin EST 530
117 8.4 42.0 11 1 ABV72108 Human skin EST 989
118 8.4 42.0 11 1 ABV62632 Human skin EST 418
119 8.4 42.0 11 1 ABV65381 Human skin EST 316
120 8.4 42.0 11 1 ABV67446 Human skin EST 523
121 8.4 42.0 11 1 ABV66204 Human skin EST 399
122 8.4 42.0 11 1 ABV65314 Human skin EST 310
123 8.4 42.0 11 1 ABV70072 Human skin EST 785
124 8.4 42.0 11 1 ABV69202 Human skin EST 698
125 8.4 42.0 11 1 ABV70053 Human skin EST 783
126 8.4 42.0 11 1 ADG88256 A. thaliana pathog
127 8.4 42.0 11 1 ADX41823 Human MN gene intr
128 8.4 42.0 11 1 ADX35643 Human hair-bearing
129 8.4 42.0 11 1 ADX35785 Human hair-bearing
130 8.4 42.0 11 1 ADX34760 Human facial skin-
131 8.4 42.0 11 1 ADX32076 Human facial skin-
132 8.4 42.0 11 1 ADX34356 Human facial skin-
133 8.4 42.0 11 1 ADX34361 Human facial skin-
134 8.4 42.0 11 1 ADX33229 Human facial skin-
135 8.4 42.0 11 1 ADX32097 Human facial skin-
136 8.4 42.0 8 1 AAT09397 5'-primer used for
137 8.4 42.0 8 1 AAT09546 3'-primer used for
138 8.4 42.0 8 1 AAT09415 3'-primer used for
139 8.4 42.0 8 1 AAT09568 Zinc finger protei
140 8.4 42.0 9 1 ABO71965 Zinc finger protei
141 8.4 42.0 9 1 ABO71964 Zinc finger protei
142 8.4 42.0 9 1 ABO71781 Zinc finger protei
143 8.4 42.0 9 1 ABO71780 Zinc finger protei
144 8.4 42.0 9 1 ACD06034 Human VEGF-targete
145 8.4 42.0 9 1 ACD19256 Human VEGF-targete
146 8.4 42.0 9 1 ADA64108 Zinc finger target
147 8.4 42.0 9 1 ADA64291 Zinc finger target
148 8.4 42.0 9 1 ADA64292 Zinc finger target
149 8.4 42.0 9 1 ADA64107 Zinc finger target
150 8.4 42.0 9 1 ADM22799 Synthetic zinc fin
151 8.4 42.0 9 1 ADM22984 Synthetic zinc fin
152 8.4 42.0 9 1 ADM22983 Synthetic zinc fin
153 8.4 42.0 9 1 ADM22800 Synthetic zinc fin
154 8.4 42.0 10 1 AAZ79378 Human dendritic ce
155 8.4 42.0 10 1 AAZ77868 Human dendritic ce
156 8.4 42.0 10 1 AAZ78273 Human dendritic ce
157 8.4 42.0 10 1 AAZ78942 Human dendritic ce
158 8.4 42.0 10 1 AAZ77770 Human dendritic ce
159 8.4 42.0 10 1 AAZ77870 Human dendritic ce
160 8.4 42.0 10 1 AAZ79364 Human dendritic ce
161 8.4 42.0 10 1 AAZ79551 Human dendritic ce
162 8.4 42.0 10 1 AAZ83134 Metastatic breast
163 8.4 42.0 10 1 AAZ81919 Metastatic breast
164 8.4 42.0 10 1 AAZ84193 Metastatic breast
165 8.4 42.0 10 1 AAZ82122 Metastatic breast
166 8.4 42.0 10 1 AAZ83647 Metastatic breast
167 8.4 42.0 10 1 AAZ83418 Metastatic breast
168 8.4 42.0 10 1 AAZ82784 Metastatic breast
169 8.4 42.0 10 1 AAZ85883 Metastatic breast
170 8.4 42.0 10 1 AAZ86535 Metastatic breast
171 8.4 42.0 10 1 AAZ81064 Metastatic breast
172 8.4 42.0 10 1 AAZ83286 Metastatic breast
173 8.4 42.0 10 1 AAZ84897 Metastatic breast
174 8.4 42.0 10 1 AAZ81128 Metastatic breast
175 8.4 42.0 10 1 AAZ83682 Metastatic breast
176 8.4 42.0 10 1 AAZ83851 Metastatic breast
177 8.4 42.0 10 1 AAZ79914 Human dendritic ce
178 8.4 42.0 10 1 AAH64317 Human ubiquitously
179 8.4 42.0 10 1 AAH63292 Human colon epithel

```

```

180 8 40.0 10 1 AAF69638 Human IL4Ra1pha ge
181 8 40.0 10 1 AAF35751 Yeast NORF gene SA
182 8 40.0 10 1 AAF39472 Yeast NORF gene SA
183 8 40.0 10 1 AAF39102 Yeast NORF gene SA
184 8 40.0 10 1 AAF41579 Yeast NORF gene SA
185 8 40.0 10 1 AAF43940 Yeast NORF gene SA
186 8 40.0 10 1 AAF34735 Yeast NORF gene SA
187 8 40.0 10 1 AAF344229 Yeast NORF gene SA
188 8 40.0 10 1 AAF37328 Yeast NORF gene SA
189 8 40.0 10 1 ABR24258 Retinaldehyde-bind
190 8 40.0 10 1 ABR23697 Transcript tag DNA
191 8 40.0 10 1 AAS16818 Human apolipoprote
192 8 40.0 10 1 ADC09948 Optical nucleic ac
193 8 40.0 10 1 ADI13743 Cytoplasmic tumour
194 8 40.0 10 1 ADK13070 Human glioma endot
195 8 40.0 10 1 ADM57243 A thaliana herbici

```

ALIGNMENTS

```

RESULT 1
ID AAL62417/c
ID AAL62417 standard, DNA, 20 BP.
XX AC AAL62417;
XX AC 06-OCT-2003 (first entry)
DE Human ABC transporter MHC I antisense oligonucleotide, ISIS 206598.
XX KM ABC transporter; ABCT, major histocompatibility complex; MHC; cytostatic;
XX KM hyperproliferative; autoimmune disorder; antisense gene therapy;
XX KM inflammation; tumour formation; immunosuppressive; antimicrobial; human;
XX KM phosphorothioate backbone; antisense; ss.
XX OS Homo sapiens.
XX OS Synthetic.
XX XX Location/Qualifiers
XX FH Key modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "Phosphorothioate backbone; All cytidines are 5-
XX FT methylcytidines"
XX FT modified_base 1..5
XX FT /tag= b
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotides"
XX FT modified_base 16..20
XX FT /tag= c
XX FT /mod_base= OTHER
XX FT /note= "2'-methoxyethyl nucleotides"
XX XX
XX XX W02003051309-A2.
XX XX 26-JUN-2003.
XX XX 12-DEC-2002; 2002WO-US040101.
XX XX 17-DEC-2001; 2001US-00024369.
XX XX (ISIS-) ISIS PHARM INC.
XX XX Borchers AH, Ward DT, Freier SM;
XX XX WPI; 2003-577305/54.
XX XX New antisense compound that hybridizes and inhibits the nucleic acid
XX XX encoding ABC transporter major histocompatibility complex 1, for treating
XX XX diseases or conditions such as a hyperproliferative or autoimmune
XX XX disorder.

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:40:33 : Search time 0.001 seconds
(without alignments)
83.680 Million cell updates/sec

Title: us-10-024-369-3
Perfect score: 20
Sequence: 1 cctctgcccaagaaggtgsg 20

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 195 seqs, 2092 residues

Total number of hits satisfying chosen parameters: 390

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 195 summaries

Database: rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	20	1	AA162417	Human ABC transpor
2	12	60.0	15	ABA96458	Human IL-2 probe S
3	11.8	59.0	15	AA45927	IGFBP2 oligonucleo
4	11.4	57.0	15	AA45927	IGFBP2 oligonucleo
5	11.4	57.0	15	AA45928	IGFBP2 oligonucleo
6	11	55.0	13	ABC34320	Oligonucleotide SE
7	11	55.0	13	ABC43321	Oligonucleotide SE
8	11	55.0	13	ABC45615	Oligonucleotide SE
9	11	55.0	13	ABC45615	Oligonucleotide SE
10	10	50.0	10	AA281481	Metastatic breast
11	10	50.0	11	ABV70040	Human skin EST 782
12	10	50.0	11	ABV62619	Human skin EST 405
13	10	50.0	12	ABH76170	Oligonucleotide pr
14	10	50.0	12	ABH71877	Oligonucleotide pr
15	10	50.0	13	AAA54180	5' exon-intron jun
16	9.8	49.0	13	ABC48640	Oligonucleotide SE
17	9.8	49.0	13	ABC48641	Oligonucleotide SE
18	9.8	49.0	13	ABF28997	Oligonucleotide SE
19	9.8	49.0	13	ABF28996	Oligonucleotide SE
20	9.4	47.0	11	ABK99486	Human facial skin-
21	9.4	47.0	11	ADQ32668	Human facial skin-
22	9.4	47.0	12	ABH13302	Oligonucleotide pr
23	9.4	47.0	12	ABH147015	Oligonucleotide pr
24	9.4	47.0	12	ABH14555	Oligonucleotide pr
25	9.4	47.0	12	ABH16922	Oligonucleotide pr
26	9.4	47.0	12	ABH91427	Oligonucleotide pr
27	9.4	47.0	12	ABH61189	Oligonucleotide pr
28	9.4	47.0	12	ABH98731	Oligonucleotide pr
29	9.4	47.0	12	ABH85586	Oligonucleotide pr
30	9.4	47.0	12	ADP78633	Chromosomal abnorm
31	9	45.0	10	AAZ79882	Human dendritic ce
32	9	45.0	10	AAZ79802	Human dendritic ce
33	9	45.0	10	AAZ78803	Human dendritic ce

34	9	45.0	10	1	AA282426	Metastatic breast
35	9	45.0	10	1	AA242275	Yeast NORF gene SA
36	9	45.0	10	1	ABT14287	Nucleic acid PCR a
37	9	45.0	10	1	ADQ38610	Human CBR gene al
38	9	45.0	11	1	AA487795	Promoter P15B3 tra
39	9	45.0	11	1	AA507926	Human transcrip tio
40	9	45.0	11	1	ABV64418	Human skin EST 220
41	9	45.0	11	1	ABV71839	Human skin EST 962
42	9	45.0	11	1	AAK99270	P15B4 promoter tra
43	9	45.0	11	1	AA281210	Transmissible gast
44	9	45.0	11	1	ADQ30775	Oligonucleotide pr
45	9	45.0	11	1	ADQ33660	Human facial skin-
46	9	45.0	12	1	ABH19388	Oligonucleotide pr
47	9	45.0	12	1	ABH108577	Oligonucleotide pr
48	9	45.0	12	1	ABH25588	Oligonucleotide pr
49	9	45.0	12	1	ABH13144	Oligonucleotide pr
50	9	45.0	12	1	ABH18769	Oligonucleotide pr
51	9	45.0	12	1	ABH88612	Oligonucleotide pr
52	9	45.0	12	1	ABH67143	Oligonucleotide pr
53	9	45.0	12	1	ABH94365	Oligonucleotide pr
54	9	45.0	12	1	ABH96358	Oligonucleotide pr
55	9	45.0	12	1	ABH74429	Oligonucleotide pr
56	9	45.0	12	1	ABH70993	Oligonucleotide pr
57	9	45.0	12	1	ABH88613	Oligonucleotide pr
58	9	45.0	12	1	ABH2693	Oligonucleotide pr
59	9	45.0	12	1	ABH10468	Oligonucleotide pr
60	9	45.0	12	1	ABH10163	Oligonucleotide pr
61	9	45.0	12	1	ABH94363	Oligonucleotide pr
62	9	45.0	12	1	ABH73341	Oligonucleotide pr
63	9	45.0	12	1	AA25619	MILC5L LNA probe
64	9	45.0	12	1	AA25617	MILC5P PNA probe
65	9	45.0	12	1	ADP28540	Human secreted pro
66	9	45.0	12	1	AA714161	Cytokine responsiv
67	8.4	42.0	10	1	AAV56888	Regulatory element
68	8.4	42.0	10	1	AAZ79653	Human dendritic ce
69	8.4	42.0	10	1	AAZ77834	Human dendritic ce
70	8.4	42.0	10	1	AAZ78009	Human dendritic ce
71	8.4	42.0	10	1	AAZ84938	Metastatic breast
72	8.4	42.0	10	1	AAZ85708	Metastatic breast
73	8.4	42.0	10	1	AAZ81181	Metastatic breast
74	8.4	42.0	10	1	AAZ80869	Metastatic breast
75	8.4	42.0	10	1	AAZ79893	Probe #25 for sequ
76	8.4	42.0	10	1	AAH63873	Human dendritic ce
77	8.4	42.0	10	1	AAH63873	Human dendritic ce
78	8.4	42.0	10	1	AAH43792	Human ubiquitously
79	8.4	42.0	10	1	AAH34723	Yeast NORF gene SA
80	8.4	42.0	10	1	AAH38664	Yeast NORF gene SA
81	8.4	42.0	10	1	AAH31520	Yeast NORF gene SA
82	8.4	42.0	10	1	AAH37547	Yeast NORF gene SA
83	8.4	42.0	10	1	AAH40919	Yeast NORF gene SA
84	8.4	42.0	10	1	AAH38810	Yeast NORF gene SA
85	8.4	42.0	10	1	AAH41899	Yeast NORF gene SA
86	8.4	42.0	10	1	AAH40814	Yeast NORF gene SA
87	8.4	42.0	10	1	ABH88354	Human CHNE gene p
88	8.4	42.0	10	1	ABH39516	Human ALA52 gene a
89	8.4	42.0	10	1	ABH139516	Human E7B3 primer-
90	8.4	42.0	10	1	ABL52253	Human PKG2 prefer
91	8.4	42.0	10	1	ABL52252	Human PKG2 prefer
92	8.4	42.0	10	1	ABV78454	Human transcrip tio
93	8.4	42.0	10	1	ABV84246	Human mitochondria
94	8.4	42.0	10	1	ABK23703	Transcript tag DNA
95	8.4	42.0	10	1	ABN84506	Rat smooth muscle
96	8.4	42.0	10	1	ACA60848	Rat smooth muscle
97	8.4	42.0	10	1	ABQ72900	Human GRN9 gene po
98	8.4	42.0	10	1	ABK65537	Human PAV gene, p
99	8.4	42.0	10	1	ACF04526	Stuffer sequence u
100	8.4	42.0	10	1	ADH13685	Cytoplasmic tumour
101	8.4	42.0	10	1	ADH13685	Human TAT protein-
102	8.4	42.0	10	1	ADM33249	Oligo SEQ ID 84, u
103	8.4	42.0	11	1	AAA16595	Human MN gene 5', d
104	8.4	42.0	11	1	AAA52514	Human MN gene intr
105	8.4	42.0	11	1	ABO87504	Human skin stress/
106	8.4	42.0	11	1	ABQ87500	Human skin stress/

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OW nucleic - nucleic search, using sw model

Run on: December 3, 2004, 11:38:34 ; Search time 0.001 Seconds

(without alignments)
37.240 Million cell updates/sec

Title: us-10-024-369-3

Perfect score: 20
Sequence: 1 cttccgcccaagaagtg95 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 88 seqs, 931 residues

Total number of hits satisfying chosen parameters: 176

Minimum DB seq length: 8

Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 88 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	12	60.0	15	1	BD061440
C 2	10	50.0	11	1	ACCESSTION:AX623364
C 3	10	50.0	11	1	ACCESSTION:AX630785
C 4	9.4	47.0	11	1	ACCESSTION:CO835700
C 5	9.4	47.0	11	1	AX472203
C 6	9	45.0	10	1	BD238992
C 7	9	45.0	10	1	BD239512
C 8	9	45.0	10	1	BD239813
C 9	9	45.0	11	1	CO836692
C 10	9	45.0	11	1	AR353840
C 11	9	45.0	11	1	AX625163
C 12	9	45.0	11	1	AX625163
C 13	9	45.0	12	1	AR349259
C 14	9	45.0	12	1	AR349251
C 15	8.4	42.0	10	1	AR92569
C 16	8.4	42.0	10	1	AR043677
C 17	8.4	42.0	10	1	BD238844
C 18	8.4	42.0	10	1	BD239019
C 19	8.4	42.0	10	1	BD240663
C 20	8.4	42.0	10	1	CO766709
C 21	8.4	42.0	10	1	AR303500
C 22	8.4	42.0	10	1	AX152798
C 23	8.4	42.0	10	1	AX301616
C 24	8.4	42.0	10	1	AX374630
C 25	8.4	42.0	10	1	AX805907
C 26	8.4	42.0	10	1	BD161343
C 27	8.4	42.0	10	1	BD165511
C 28	8.4	42.0	11	1	AR074494
C 29	8.4	42.0	11	1	AR081174
C 30	8.4	42.0	11	1	AR085171
C 31	8.4	42.0	11	1	AR088119
C 32	8.4	42.0	11	1	AR104278
C 33	8.4	42.0	11	1	AR143540

34	8.4	42.0	11	1	AR171446	ACCESSTION:AR171446
35	8.4	42.0	11	1	AR171617	ACCESSTION:AR171617
36	8.4	42.0	11	1	BD243207	ACCESSTION:BD243207
C 37	8.4	42.0	11	1	CO833089	ACCESSTION:CO833089
C 38	8.4	42.0	11	1	CO833231	ACCESSTION:CO833231
C 39	8.4	42.0	11	1	CO835108	ACCESSTION:CO835108
C 40	8.4	42.0	11	1	CO835129	ACCESSTION:CO835129
C 41	8.4	42.0	11	1	CO836261	ACCESSTION:CO836261
C 42	8.4	42.0	11	1	CO837368	ACCESSTION:CO837368
C 43	8.4	42.0	11	1	CO837393	ACCESSTION:CO837393
C 44	8.4	42.0	11	1	CO837792	ACCESSTION:CO837792
C 45	8.4	42.0	11	1	134822	ACCESSTION:134822
C 46	8.4	42.0	11	1	AX412934	ACCESSTION:AX412934
C 47	8.4	42.0	11	1	AX470593	ACCESSTION:AX470593
C 48	8.4	42.0	11	1	AX471678	ACCESSTION:AX471678
C 49	8.4	42.0	11	1	AX471682	ACCESSTION:AX471682
C 50	8.4	42.0	11	1	AX623377	ACCESSTION:AX623377
C 51	8.4	42.0	11	1	AX623396	ACCESSTION:AX623396
C 52	8.4	42.0	11	1	AX623509	ACCESSTION:AX623509
C 53	8.4	42.0	11	1	AX625581	ACCESSTION:AX625581
C 54	8.4	42.0	11	1	AX626059	ACCESSTION:AX626059
C 55	8.4	42.0	11	1	AX626126	ACCESSTION:AX626126
C 56	8.4	42.0	11	1	AX626949	ACCESSTION:AX626949
C 57	8.4	42.0	11	1	AX627089	ACCESSTION:AX627089
C 58	8.4	42.0	11	1	AX627751	ACCESSTION:AX627751
C 59	8.4	42.0	11	1	AX627792	ACCESSTION:AX627792
C 60	8.4	42.0	11	1	AX627837	ACCESSTION:AX627837
C 61	8.4	42.0	11	1	AX628191	ACCESSTION:AX628191
C 62	8.4	42.0	11	1	AX628263	ACCESSTION:AX628263
C 63	8.4	42.0	11	1	AX629947	ACCESSTION:AX629947
C 64	8.4	42.0	11	1	AX630798	ACCESSTION:AX630798
C 65	8.4	42.0	11	1	AX630817	ACCESSTION:AX630817
C 66	8.4	42.0	11	1	AX630930	ACCESSTION:AX630930
C 67	8.4	42.0	11	1	AX632853	ACCESSTION:AX632853
C 68	8.4	42.0	9	1	AX480947	ACCESSTION:AX480947
C 69	8.4	42.0	9	1	AX668629	ACCESSTION:AX668629
C 70	8.4	42.0	9	1	AX668630	ACCESSTION:AX668630
C 71	8.4	42.0	9	1	AX668813	ACCESSTION:AX668813
C 72	8.4	42.0	9	1	AX668814	ACCESSTION:AX668814
C 73	8.4	42.0	9	1	AB012724	ACCESSTION:AB012724
C 74	8.4	42.0	10	1	AX15662	ACCESSTION:AX15662
C 75	8.4	42.0	10	1	BD238780	ACCESSTION:BD238780
C 76	8.4	42.0	10	1	BD238878	ACCESSTION:BD238878
C 77	8.4	42.0	10	1	BD238880	ACCESSTION:BD238880
C 78	8.4	42.0	10	1	BD239283	ACCESSTION:BD239283
C 79	8.4	42.0	10	1	BD239952	ACCESSTION:BD239952
C 80	8.4	42.0	10	1	BD240374	ACCESSTION:BD240374
C 81	8.4	42.0	10	1	BD240388	ACCESSTION:BD240388
C 82	8.4	42.0	10	1	BD240561	ACCESSTION:BD240561
C 83	8.4	42.0	10	1	119168	ACCESSTION:119168
C 84	8.4	42.0	10	1	119170	ACCESSTION:119170
C 85	8.4	42.0	10	1	AR303345	ACCESSTION:AR303345
C 86	8.4	42.0	10	1	AX152217	ACCESSTION:AX152217
C 87	8.4	42.0	10	1	AX153242	ACCESSTION:AX153242
C 88	8.4	42.0	10	1	AX301610	ACCESSTION:AX301610

ALIGNMENTS

RESULT 1
LOCUS BD061440/c
DEFINITION Method for selectively separating living cell expressed with
specific gene.
ACCESSION BD061440
VERSION BD061440.1 GI:22607046
KEYWORDS JP 2001286285-A/2.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 15)
AUTHORS Ishibashi, K. and Tsuji, A.